

V. PORTNER

1641

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/259,658

DATE: 05/18/2000
TIME: 14:10:57

Input Set : A:\Sequence.lst
Output Set: N:\CRF3\05182000\I259658.raw

3 <110> APPLICANT: Colyer
4 Craig
5 Maschio
6 Mezna
8 <120> TITLE OF INVENTION: Compositions And Methods For Monitoring The
9 Modification State Of A Pair Of Polypeptides
11 <130> FILE REFERENCE: colyer 4256/79245
13 <140> CURRENT APPLICATION NUMBER: 09/259,658
14 <141> CURRENT FILING DATE: 1999-02-26
16 <160> NUMBER OF SEQ ID NOS: 59
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 43
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence:Protein binding
27 motif.
29 <400> SEQUENCE: 1
30 His His His His His His Gly Gly Ile Ala Gln Leu Glu Gln Glu Ile
31 1 5 10 15
33 Ala Gln Leu Glu Gln Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln
34 20 25 30
36 Leu Glu Gln Glu Ile Ala Lys Leu Glu Gln Glu
37 35 40
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 35
42 <212> TYPE: PRT
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence:Protein binding
47 motif.
49 <400> SEQUENCE: 2
50 Ile Ala Gln Leu Lys Gln Lys Ile Ala Gln Leu Lys Gln Lys Asn Ala
51 1 5 10 15
53 Gln Leu Lys Gln Lys Ile Ala Gln Leu Lys Gln Lys Ile Cys Gln Leu
54 20 25 30
56 Lys Gln Lys
57 35
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 5
62 <212> TYPE: PRT
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence:Protein binding
67 motif.
69 <220> FEATURE:

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70 <221> NAME/KEY: SITE
 71 <222> LOCATION: (2)
 72 <223> OTHER INFORMATION: Xaa at position 2 can be any amino acid.
 74 <400> SEQUENCE: 3
 75 Tyr Xaa Asp Glu Asp
 76 1 5
 79 <210> SEQ ID NO: 4
 80 <211> LENGTH: 41
 81 <212> TYPE: PRT
 82 <213> ORGANISM: Homo sapiens
 84 <400> SEQUENCE: 4
 85 Ile Leu Ile Ser Leu Glu Ser Glu Glu Arg Gly Glu Leu Glu Arg Ile
 86 1 5 10 15
 88 Leu Ala Asp Leu Glu Glu Glu Asn Arg Asn Leu Gln Ala Glu Tyr Asp
 89 20 25 30
 91 Arg Leu Lys Gln Gln His Glu His Lys
 92 35 40
 95 <210> SEQ ID NO: 5
 96 <211> LENGTH: 32
 97 <212> TYPE: PRT
 98 <213> ORGANISM: Saccharomyces cerevisiae
 100 <400> SEQUENCE: 5
 101 Met Lys Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr
 102 1 5 10 15
 104 His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
 105 20 25 30
 111 <210> SEQ ID NO: 6
 112 <211> LENGTH: 39
 113 <212> TYPE: PRT
 114 <213> ORGANISM: Homo sapiens
 116 <400> SEQUENCE: 6
 117 Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
 118 1 5 10 15
 120 Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
 121 20 25 30
 123 Glu Phe Ile Leu Ala Ala His
 124 35
 127 <210> SEQ ID NO: 7
 128 <211> LENGTH: 39
 129 <212> TYPE: PRT
 130 <213> ORGANISM: Homo sapiens
 132 <400> SEQUENCE: 7
 133 Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser
 134 1 5 10 15
 136 Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu
 137 20 25 30
 139 Lys Gln Lys Val Met Asn His
 140 35
 143 <210> SEQ ID NO: 8

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144 <211> LENGTH: 38
145 <212> TYPE: PRT
146 <213> ORGANISM: Escherichia coli
148 <400> SEQUENCE: 8
149 Val Asp Lys Leu Gly Ala Leu Glu Glu Arg Arg Lys Val Leu Gln Val
150   1           5           10           15
152 Lys Thr Glu Asn Leu Gln Ala Glu Arg Asn Ser Arg Ser Lys Ser Ile
153           20           25           30
155 Gly Gln Ala Lys Ala Arg
156           35
159 <210> SEQ ID NO: 9
160 <211> LENGTH: 32
161 <212> TYPE: PRT
162 <213> ORGANISM: Escherichia coli
164 <400> SEQUENCE: 9
165 Glu Pro Leu Arg Leu Glu Val Asn Lys Leu Gly Glu Glu Leu Asp Ala
166   1           5           10           15
168 Ala Lys Ala Glu Leu Asp Ala Leu Gln Ala Glu Ile Arg Asp Ile Ala
169           20           25           30
175 <210> SEQ ID NO: 10
176 <211> LENGTH: 33
177 <212> TYPE: PRT
178 <213> ORGANISM: Thermus thermophilus
180 <400> SEQUENCE: 10
181 Asp Leu Glu Ala Leu Leu Ala Leu Asp Arg Glu Val Gln Glu Leu Lys
182   1           5           10           15
184 Lys Arg Leu Gln Glu Val Gln Thr Glu Arg Asn Gln Val Ala Lys Arg
185           20           25           30
187 Val
191 <210> SEQ ID NO: 11
192 <211> LENGTH: 32
193 <212> TYPE: PRT
194 <213> ORGANISM: Thermus thermophilus
196 <400> SEQUENCE: 11
197 Glu Ala Leu Ile Ala Arg Gly Lys Ala Leu Gly Glu Glu Ala Lys Arg
198   1           5           10           15
200 Leu Glu Glu Ala Leu Arg Glu Lys Glu Ala Arg Leu Glu Ala Leu Leu
201           20           25           30
207 <210> SEQ ID NO: 12
208 <211> LENGTH: 30
209 <212> TYPE: PRT
210 <213> ORGANISM: Escherichia coli
212 <400> SEQUENCE: 12
213 Leu Arg Gly Ala Glu Lys Leu Arg Glu Glu Leu Asp Phe Leu Lys Ser
214   1           5           10           15
216 Val Phe Arg Pro Glu Ile Ile Ala Ala Ile Ala Glu Ala Arg
217           20           25           30
220 <210> SEQ ID NO: 13
221 <211> LENGTH: 26

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222 <212> TYPE: PRT
223 <213> ORGANISM: Escherichia coli
225 <400> SEQUENCE: 13
226 Ala Glu Tyr His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg
227   1           5           10           15
229 Ile Lys Asp Ile Glu Ala Lys Leu Ser Asn
230           20           25
233 <210> SEQ ID NO: 14
234 <211> LENGTH: 32
235 <212> TYPE: PRT
236 <213> ORGANISM: Saccharomyces cerevisiae
238 <400> SEQUENCE: 14
239 Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr
240   1           5           10           15
242 His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg
243           20           25           30
249 <210> SEQ ID NO: 15
250 <211> LENGTH: 29
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic
256     peptide for coiled coil protein binding.
258 <400> SEQUENCE: 15
259 Glu Trp Glu Ala Leu Glu Lys Lys Leu Ala Ala Leu Glu Ser Lys Leu
260   1           5           10           15
262 Gln Ala Leu Glu Lys Lys Leu Glu Ala Leu Glu His Gly
263           20           25
266 <210> SEQ ID NO: 16
267 <211> LENGTH: 32
268 <212> TYPE: PRT
269 <213> ORGANISM: Saccharomyces cerevisiae
271 <400> SEQUENCE: 16
272 Met Lys Gln Ile Glu Asp Lys Leu Glu Glu Ile Leu Ser Lys Leu Tyr
273   1           5           10           15
275 His Ile Glu Asn Glu Leu Ala Arg Ile Lys Lys Leu Leu Gly Glu Arg
276           20           25           30
282 <210> SEQ ID NO: 17
283 <211> LENGTH: 25
284 <212> TYPE: PRT
285 <213> ORGANISM: Escherichia coli
287 <400> SEQUENCE: 17
288 Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile Arg Ser Gln Thr
289   1           5           10           15
291 Leu Thr Leu Leu Glu Lys Leu Asn Glu
292           20           25
295 <210> SEQ ID NO: 18
296 <211> LENGTH: 24
297 <212> TYPE: PRT

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Input Set : A:\Sequence.lst
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298 <213> ORGANISM: Escherichia coli
 300 <400> SEQUENCE: 18
 301 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
 302 1 5 10 15
 304 Leu Tyr Arg Ser Cys Leu Ala Arg
 305 20
 308 <210> SEQ ID NO: 19
 309 <211> LENGTH: 16
 310 <212> TYPE: PRT
 311 <213> ORGANISM: Homo sapiens
 313 <400> SEQUENCE: 19
 314 Leu Ile Leu Ile Cys Leu Leu Leu Ile Cys Ile Ile Val Met Leu Leu
 315 1 5 10 15
 318 <210> SEQ ID NO: 20
 319 <211> LENGTH: 5
 320 <212> TYPE: PRT
 321 <213> ORGANISM: Artificial Sequence
 323 <220> FEATURE:
 324 <221> NAME/KEY: SITE
 325 <222> LOCATION: (1)
 326 <223> OTHER INFORMATION: Xaa at position 1 can be W or L.
 328 <220> FEATURE:
 329 <221> NAME/KEY: SITE
 330 <222> LOCATION: (5)
 331 <223> OTHER INFORMATION: Xaa at position 5 can be any amino acid.
 333 <220> FEATURE:
 334 <223> OTHER INFORMATION: Description of Artificial Sequence:Caspase 1,4,5
 335 cleavage site.
 337 <400> SEQUENCE: 20
 338 Xaa Glu His Asp Xaa
 339 1 5
 342 <210> SEQ ID NO: 21
 343 <211> LENGTH: 5
 344 <212> TYPE: PRT
 345 <213> ORGANISM: Artificial Sequence
 347 <220> FEATURE:
 348 <221> NAME/KEY: SITE
 349 <222> LOCATION: (3)
 350 <223> OTHER INFORMATION: Xaa at position 3 can be any amino acid.
 352 <220> FEATURE:
 353 <221> NAME/KEY: SITE
 354 <222> LOCATION: (5)
 355 <223> OTHER INFORMATION: Xaa at position 5 can be any amino acid.
 357 <220> FEATURE:
 358 <223> OTHER INFORMATION: Description of Artificial Sequence:Caspase 2,3,7
 359 cleavage site.
 361 <400> SEQUENCE: 21
 362 Asp Glu Xaa Asp Xaa
 363 1 5

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/18/2000

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Input Set : A:\Sequence.lst

Output Set: N:\CRF3\05182000\I259658.raw

L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34